

Figure 1

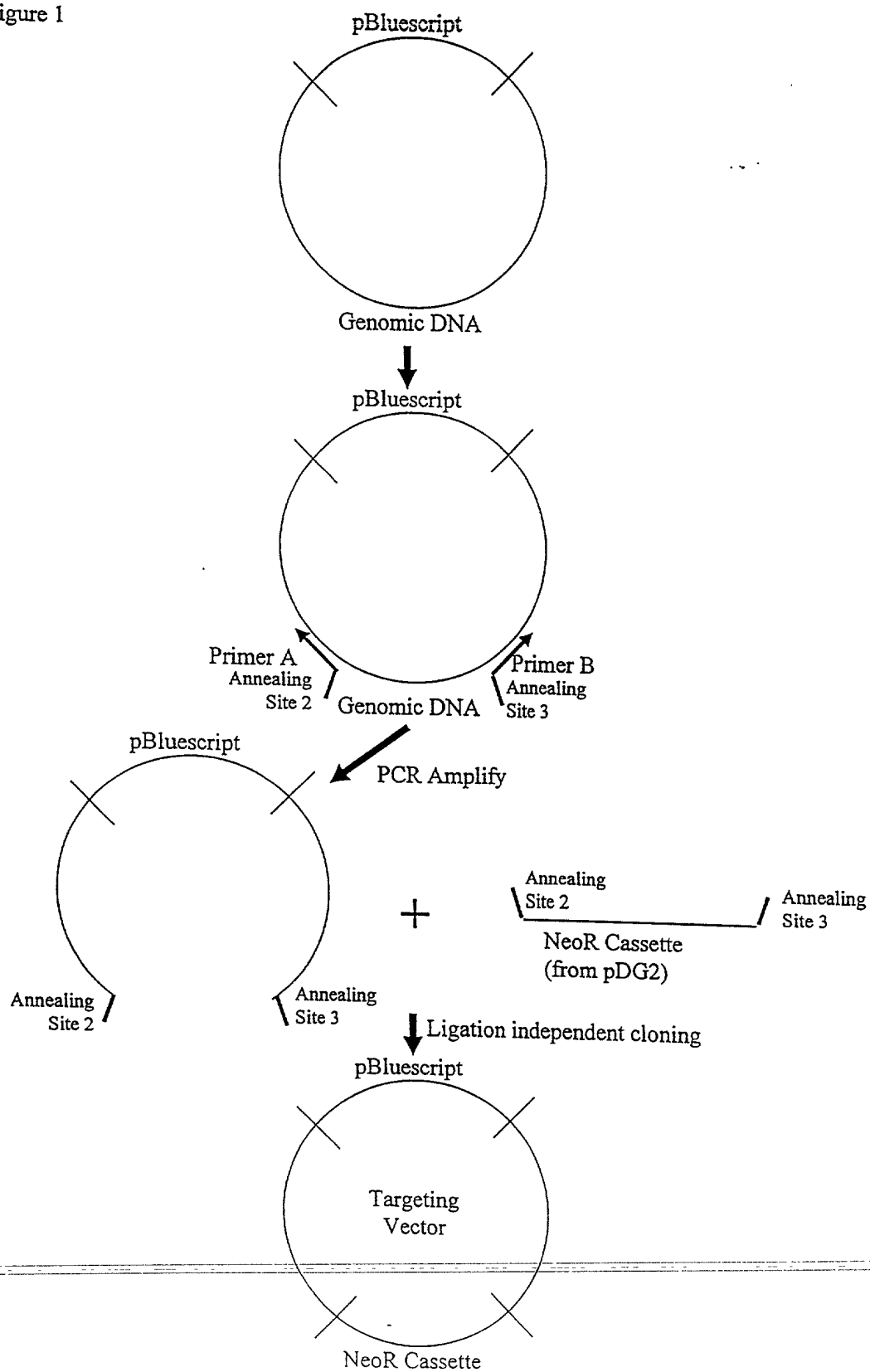
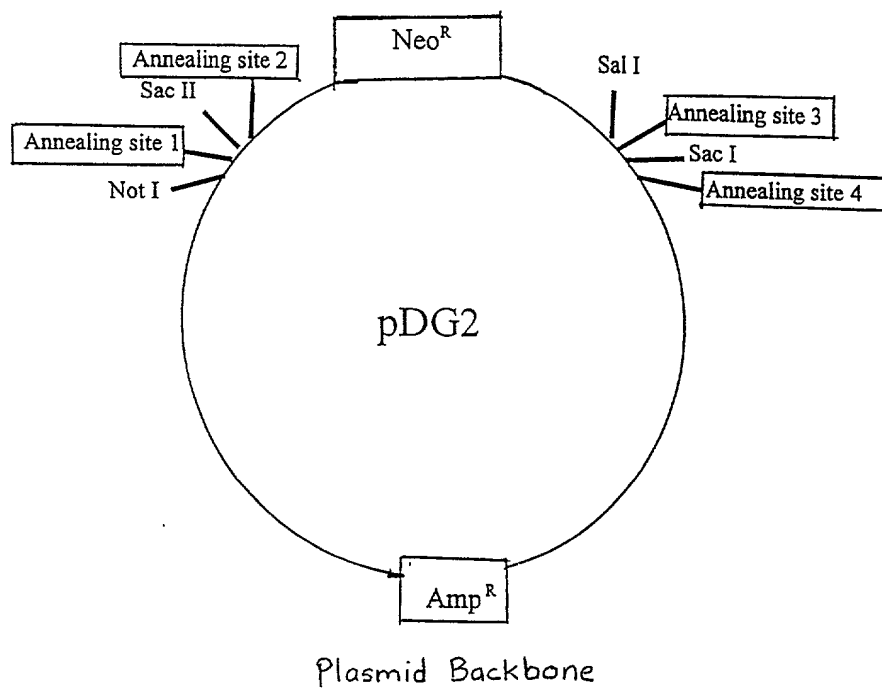


Figure 2A



pDG2:

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Fig 2B

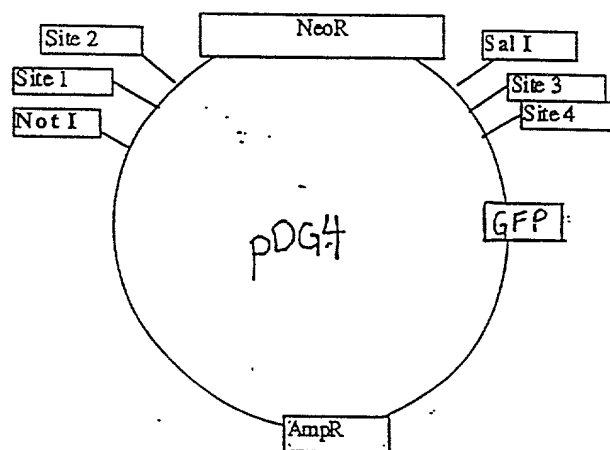


Fig 3A

[illegible]

Fig 3B

Annealing site	Sequence	Sequence after digestion
1	5' tgtgtcctcttttggttgcttccaa... 3' 3' acacgaggagaaaccgaacgaagggt... 5'	5' tgtgtcctcttttggttgcttccaa... 3' 3' tt... 5'
2	5' ctggttcttgtctggcttggcccaa... 3' 3' gaccaagaacagaccgaaccgggtt... 5'	5' ctggttcttgtctggcttggcccaa... 3' 3' tt... 5'
3	5' ggtcctcgctctgtgtccgttgaa... 3' 3' ccaggagcgagacacaggcaactt... 5'	5' ggtcctcgctctgtgtccgttgaa... 3' 3' tt... 5'
4	5' ttgcggtgtcctgtgtcgtcgaa... 3' 3' aaacgcacaggacacagcagctt... 5'	5' ttgcggtgtcctgtgtcgtcgaa... 3' 3' tt... 5'

Fig 4

Annealing site	Sequence	Sequence after digestion
1	5' AAtgtgtcctcttttggcttgcttCCGC 3' 3' Ttacacgaggagaaaccgaacgaagg 5'	5' AA 3' 3' Ttacacgaggagaaaccgaacgaagg 5'
2	5' AActgggttcttgtctggcttggcCCGC 3' 3' Ttgaccaagaacagaccgaaccggg 5'	5' AA 3' 3' Ttgaccaagaacagaccgaaccggg 5'
3	5' AAggtcctcgctctgtgtcgttGAGCT 3' 3' Ttccaggagcgagacacaggcaac 5'	5' AA 3' 3' Ttccaggagcgagaca'caggcaac 5'
4	5' AAtttgcgtgtcctgtgtcgtcGAGCT 3' 3' Ttaaacgcacaggacacagcagc 5'	5' AA 3' 3' Ttaaacgcacaggacacagcagc 5'

Fig 5

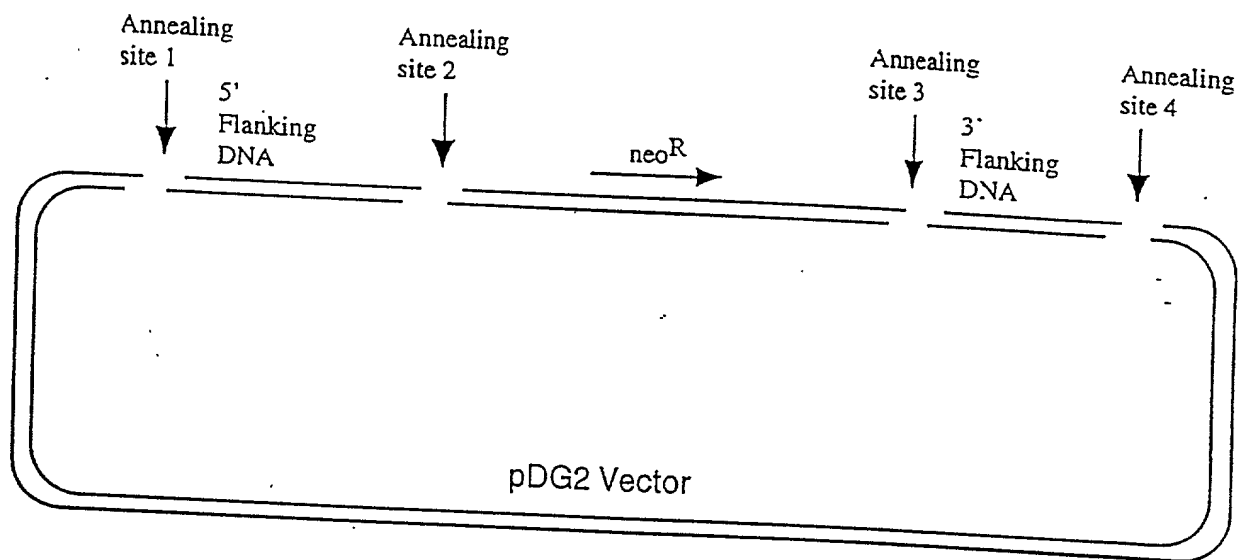


Fig 6

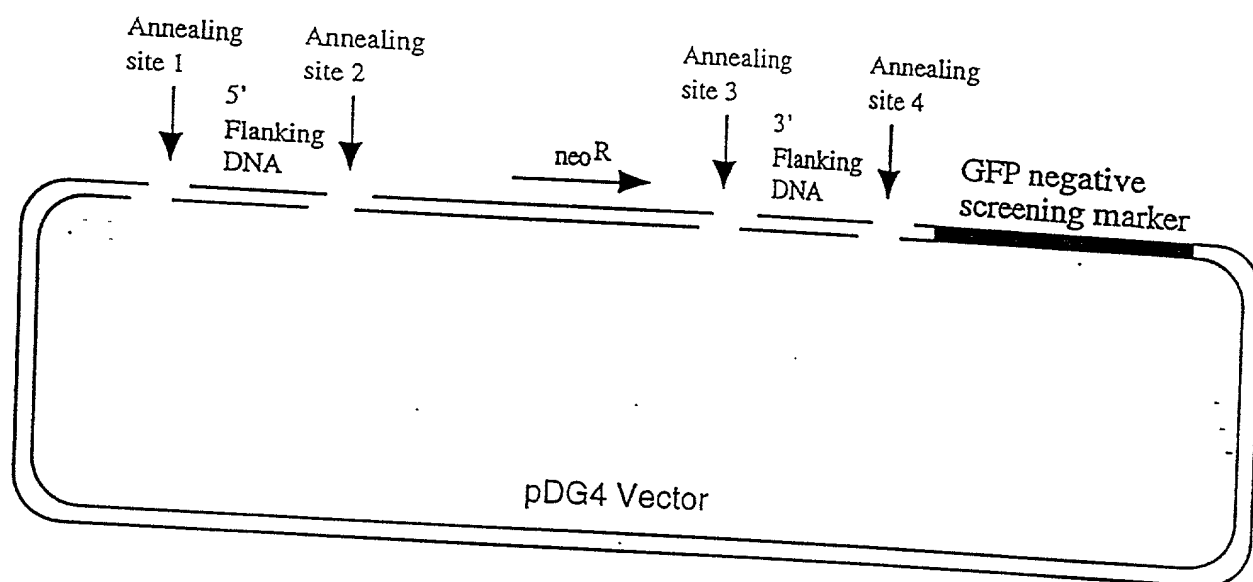


Fig 7

Oligo#	Sequence (5' to 3')
174	ATGACCGCTCAGGAAACCTGTTGCA
180	ATAGGCATAGTAGGCCAGCTTGAGG
454	tgtgctcctcttttggttgcttccAATTAACCCCTCACTAAAGGGAACGAAT
463	ctggttcttgtctggcttgcccaaTGCAACAGGTTTCCTGAGCGGTCAT
464	ggtcctcgctctgtgtccgttgaaCCTCAAGCTGGCCTACTATGCCTAT
42	tttgctgtcctgtgtcgtcgaaCGACTAATACGACTCACTATAGGGCG
151	GCCAATGGACTCTTAGTTTTGGAAC
155	GTTCTGGCAAACAAATTCGGCGCAC
454	tgtgctcctcttttggttgcttccAATTAACCCCTCACTAAAGGGAACGAAT
465	ctggttcttgtctggcttgcccaaGTCCAAACTAAGAGTCCATTGGC
466	ggtcctcgctctgtgtccgttgaaGTGCGCCGAATTTGTTTGCCAGAAC
1	GAACCTTGGTGTGCCAAGTTACTTC
2	GAACCTTGGCTGAACCCCTTGTTCT
41	tgtgctcctcttttggttgcttgaaCGACTAATACGACTCACTATAGGGCG
38	ctggttcttgtctggcttgcccaaGAAGTAACTTGGCACACCAAGGTTCT
40	ggtcctcgctctgtgtccgttgaaAGAACAAGGGGTTAGCCAAAGTTC
37	tttgctgtcctgtgtcgtcgAATTAACCCCTCACTAAAGGGAACGAAT
540	ATGCCGGATCTCCTACTACTGGGCC
546	TGTCATAGTAGACAGCGATGGAACG
445	GACAAGAACCAGTTGACGTCAAGCTTCCCGGGACGCGTGCTAGCGGCGCGCCG
667	ctggttcttgtctggcttgcccaaAGGCCAGTAGTAGGAGATCCGGCAT
668	ggtcctcgctctgtgtccgttgaaCGTTCCATCGCTGTCTACTATGACA
907	ctggttcttgtctggcttgcccaaAAAGCCGACAGCCACGCTCACAAGC
908	ggtcctcgctctgtgtccgttgaaGCCCAATGCCACAGAGACAGAATGT
1157	ctggttcttgtctggcttgcccaaGTTGGATCCTCTCCAAGGCCCATCT
1158	ggtcctcgctctgtgtccgttgaaCTCCAGTGCCGAGTGTGTGGGGACAG

Figure 8